SEQUENCE LISTING

(1) INFORMATION FOR SEQ ID NO. 1:

(i) LENGTH: 365 amino acids

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(a)ORGANISM: Candida boidinii

```
Met Gly Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala
1               5                  10                  15

Asp Glu Glu Lys Leu Tyr Gly Cys Thr Glu Asn Lys Leu Gly Ile Ala
            20                  25                  30

Asn Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys
        35                  40                  45

Glu Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile
    50                  55                  60

Ile Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu
65                  70                  75                  80

Asp Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser
                85                  90                  95

Asp His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser
            100                 105                 110

Val Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val
        115                 120                 125

Val Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu
    130                 135                 140

Gln Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala
145                 150                 155                 160

Tyr Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile
                165                 170                 175
```

```
Gly Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu
            180                 185                 190

Leu Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val
        195                 200                 205

Gly Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp
    210                 215                 220

Ile Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile
225                 230                 235                 240

Asn Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn
                245                 250                 255

Thr Ala Arg Gly Ala Ile Cys Val Ala Glu Asp Val Ala Ala Ala Leu
            260                 265                 270

Glu Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln
        275                 280                 285

Pro Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly
    290                 295                 300

Ala Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala
305                 310                 315                 320

Gln Thr Arg Tyr Ala Glu Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe
                325                 330                 335

Thr Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly
            340                 345                 350

Glu Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys
        355                 360                 365
```

(2) INFORMATION FOR SEQ ID NO. 2:

(i) LENGTH: 367 amino acids

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(a)ORGANISM: Candida boidinii

```
Met Gly Lys Ile Phe Asp Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Leu
1               5                  10                  15

Val Met Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Cys Ile
            20                  25                  30

His Val Thr Thr Leu Gly Pro Ala Leu Gly Gly Met Arg Met Trp Thr
        35                  40                  45

Tyr Ala Ser Glu Glu Glu Ala Ile Glu Asp Ala Leu Arg Leu Gly Arg
    50                  55                  60

Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly
65                  70                  75                  80

Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Asn Glu Ala Met
                85                  90                  95

Phe Arg Ala Leu Gly Arg Phe Ile Gln Gly Leu Asn Gly Arg Tyr Ile
            100                 105                 110

Thr Ala Glu Asp Val Gly Thr Thr Val Glu Asp Met Asp Ile Ile His
        115                 120                 125

Glu Glu Thr Arg Tyr Val Thr Gly Val Ser Pro Ala Phe Gly Ser Ser
    130                 135                 140

Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met Lys
145                 150                 155                 160

Ala Ala Ala Lys Glu Ala Phe Gly Asp Asp Ser Leu Glu Gly Lys Val
                165                 170                 175

Val Ala Val Gln Gly Val Gly His Val Ala Tyr Glu Leu Cys Lys His
            180                 185                 190
```

```
Leu His Asn Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys Glu
        195                 200                 205

Asn Ala Asp Arg Ala Val Gln Glu Phe Gly Ala Glu Phe Val His Pro
    210                 215                 220

Asp Lys Ile Tyr Asp Val Glu Cys Asp Ile Phe Ala Pro Cys Ala Leu
225                 230                 235                 240

Gly Ala Ile Ile Asn Asp Glu Thr Ile Glu Arg Leu Lys Cys Lys Val
                245                 250                 255

Val Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Glu Arg His Gly Lys
            260                 265                 270

Met Leu Glu Glu Lys Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn
        275                 280                 285

Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Leu Gly Tyr Asn Arg
    290                 295                 300

Glu Arg Ala Met Lys Lys Val Glu Gly Ile Tyr Asp Lys Ile Leu Lys
305                 310                 315                 320

Val Phe Glu Ile Ala Lys Arg Asp Gly Ile Pro Ser Tyr Leu Ala Ala
                325                 330                 335

Asp Arg Met Ala Glu Glu Arg Ile Glu Met Met Arg Lys Thr Arg Ser
            340                 345                 350

Thr Phe Leu Gln Asp Gln Arg Asn Leu Ile Asn Phe Asn Asn Lys
        355                 360                 365
```

(3) INFORMATION FOR SEQ ID NO. 3:

(i) LENGTH: 640 amino acids

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(a)ORGANISM: Candida boidinii

```
Met Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp Ala
1               5                  10                  15

Val Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile
            20                  25                  30

Asp Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly
        35                  40                  45

Asp Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln
    50                  55                  60

Asn Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn
65                  70                  75                  80

Gly Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn
                85                  90                  95

Trp Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr
            100                 105                 110

Lys Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val
        115                 120                 125

Ala Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile
    130                 135                 140

Asn Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly
145                 150                 155                 160

Arg Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ala
                165                 170                 175

Ile Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn
            180                 185                 190
```

```
Asp Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp
        195                 200                 205

Asp Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys
    210                 215                 220

His Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile
225                 230                 235                 240

Val Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser
                245                 250                 255

Ser Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly
            260                 265                 270

Tyr Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly
        275                 280                 285

Gly Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser
    290                 295                 300

Pro Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro
305                 310                 315                 320

Met Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala
                325                 330                 335

Trp Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser
            340                 345                 350

Thr Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser
        355                 360                 365

Ala Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys
    370                 375                 380

Gly Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe
385                 390                 395                 400

Gly Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His
                405                 410                 415

Ile Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala
            420                 425                 430
```

```
Ser Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu
        435                 440                 445

Pro Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro
    450                 455                 460

Phe Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu
465                 470                 475                 480

Gln Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Val Tyr
                485                 490                 495

His Ser Ile Ser Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly
            500                 505                 510

Gly Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile
        515                 520                 525

Phe Thr Pro Asn Tyr Leu Tyr Asn Ser Asn Gly Asn Leu Ala Thr Arg
    530                 535                 540

Pro Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg
545                 550                 555                 560

Ile Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg
                565                 570                 575

Tyr Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro
            580                 585                 590

Leu Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro
        595                 600                 605
Ser Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met
    610                 615                 620

Asn Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln
625                 630                 635                 640
```